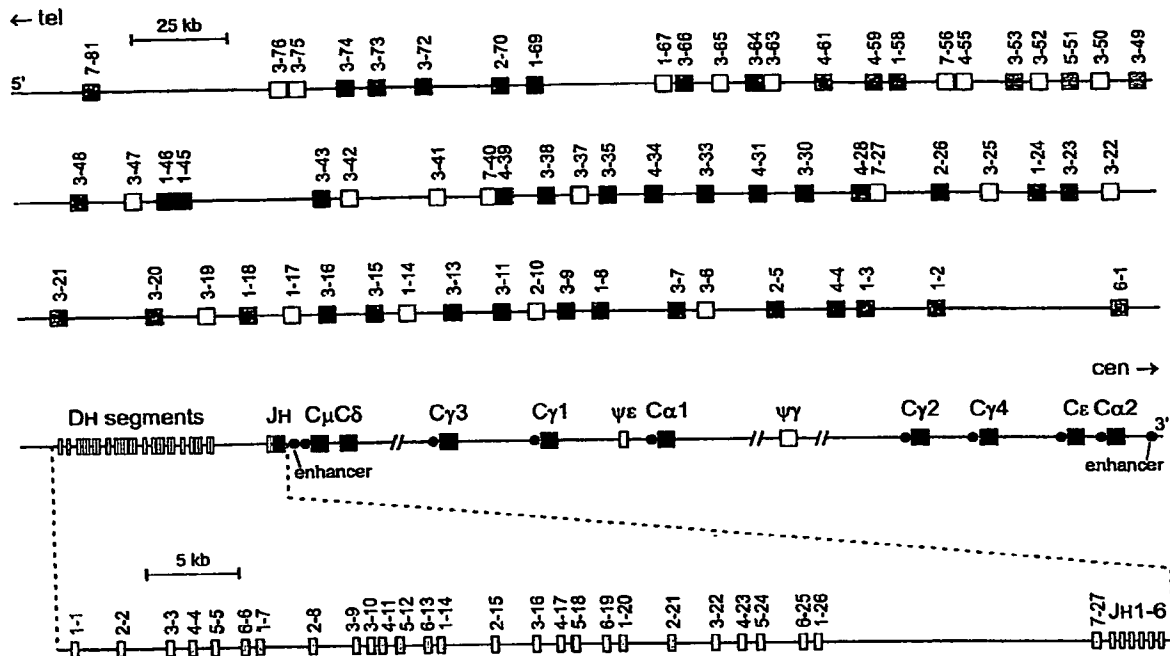
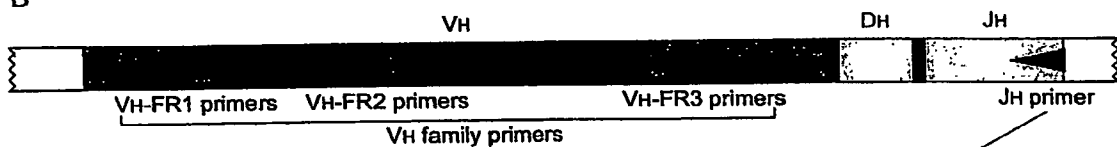


Figure 2

A. *IGH* gene complex (#14q32.3)

B



IGH tube A			5'	3'	5'	IGH tubes A, B, and C		3'
(SEQ ID NO: 1)	VH1-FR1 (1-2) (-252)	GGCCTCAGTGAAGGTCTCCTGCAAG			CCAGTGGCAGAGGAGTCCATTC	(+57)	JH consensus	(SEQ ID NO: 21)
(SEQ ID NO: 2)	VH2-FR1 (2-5) (-284)	GTCTGGTCTCTACGCTGGTGAAACCC						
(SEQ ID NO: 3)	VH3-FR1 (3-7) (-256)	CTGGGGGGTCCCTGAGACTCTCCTG						
(SEQ ID NO: 4)	VH4-FR1 (4-4) (-256)	CTTCGGAGACCCCTGTCCCTCACCTG						
(SEQ ID NO: 5)	VH5-FR1 (5-51) (-255)	CGGGGAGTCTCTGAAGATCTCCTGT						
(SEQ ID NO: 6)	VH6-FR1 (6-1) (-263)	TCGCAGACCCTCTCACTCACCTGTG						
IGH tube B			5'	3'	5'			3'
(SEQ ID NO: 7)	VH1-FR2 (1-2) (-192)	CTGGGTGCGACAGGCCCTGGACAA						
(SEQ ID NO: 8)	VH2-FR2 (2-5) (-190)	TGGATCCGTGACCCCCAGGGAAGG						
(SEQ ID NO: 9)	VH3-FR2 (3-7) (-189)	GGTCCGCCAGGCTCCAGGGAA						
(SEQ ID NO: 10)	VH4-FR2 (4-4) (-188)	TGGATCCGCCAGCCCCAGGGAAGG						
(SEQ ID NO: 11)	VH5-FR2 (5-51) (-190)	GGGTGCGCCAGATGCCCGGGAAGG						
(SEQ ID NO: 12)	VH6-FR2 (6-1) (-194)	TGGATCAGGCAGTCCCCATCGAGAG						
(SEQ ID NO: 13)	VH7-FR2 (7) (-192)	TTGGGTGCGACAGGCCCTGGACAA						
IGH tube C			5'	3'	5'			3'
(SEQ ID NO: 14)	VH1-FR3 (1-2) (-55)	TGGAGCTGAGCAGCCTGAGATCTGA						
(SEQ ID NO: 15)	VH2-FR3 (2-5) (-54)	CAATGACCAACATGGACCCTGTGGA						
(SEQ ID NO: 16)	VH3-FR3 (3-7) (-57)	TCTGCAAATGAACAGCCTGAGAGCC						
(SEQ ID NO: 17)	VH4-FR3 (4-4) (-48)	GAGCTCTGTGACCCGCGCGGACACG						
(SEQ ID NO: 18)	VH5-FR3 (5-51) (-69)	CAGCACCGCCTACCTGCAGTGGAGC						
(SEQ ID NO: 19)	VH6-FR3 (6-1) (-63)	GTTCTCCCTGCAGCTGAACTCTGTG						
(SEQ ID NO: 20)	VH7-FR3 (7) (-69)	CAGCACGGCATATCTGCAGATCAG						

Figure 3 (A and B)

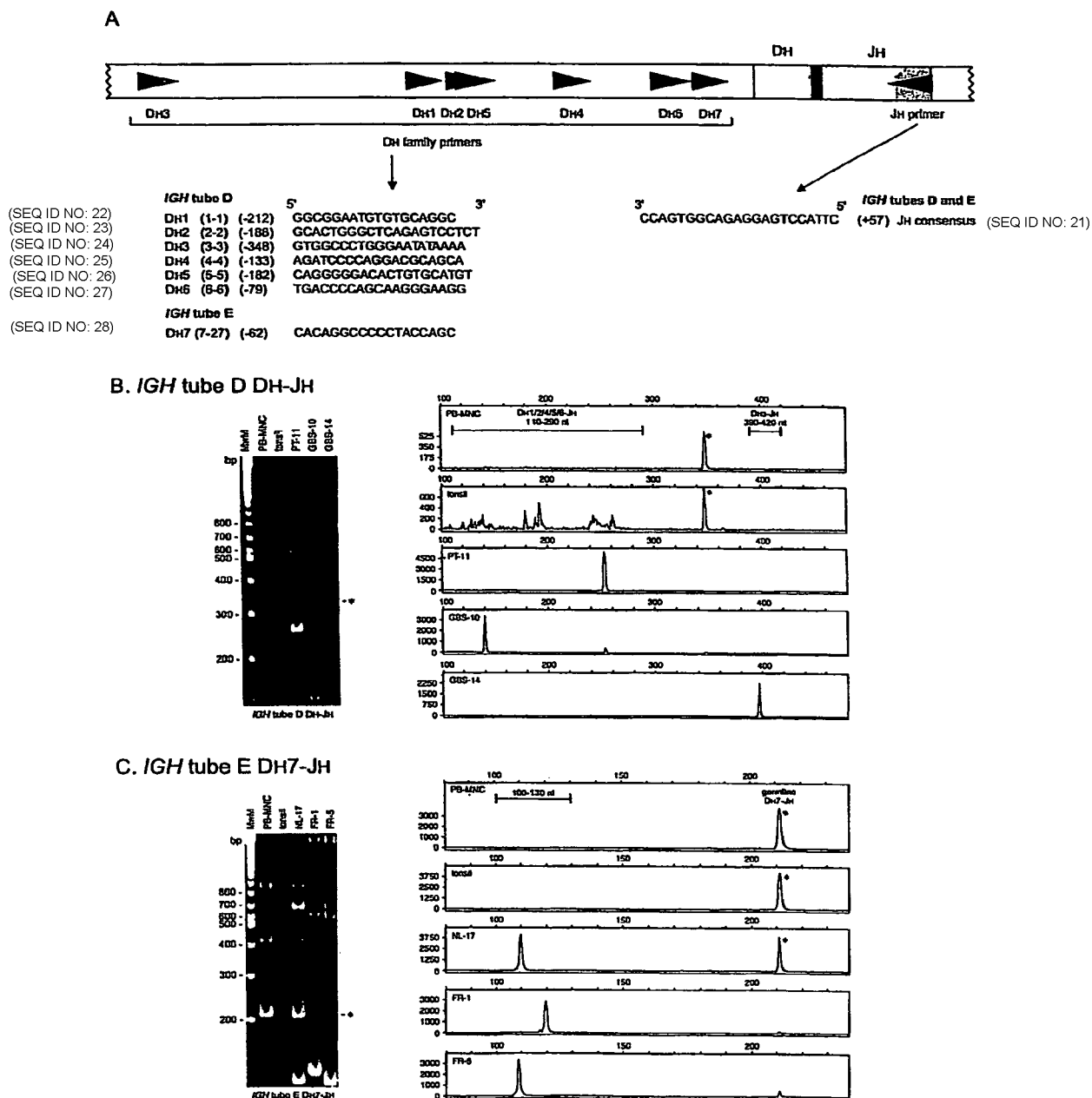
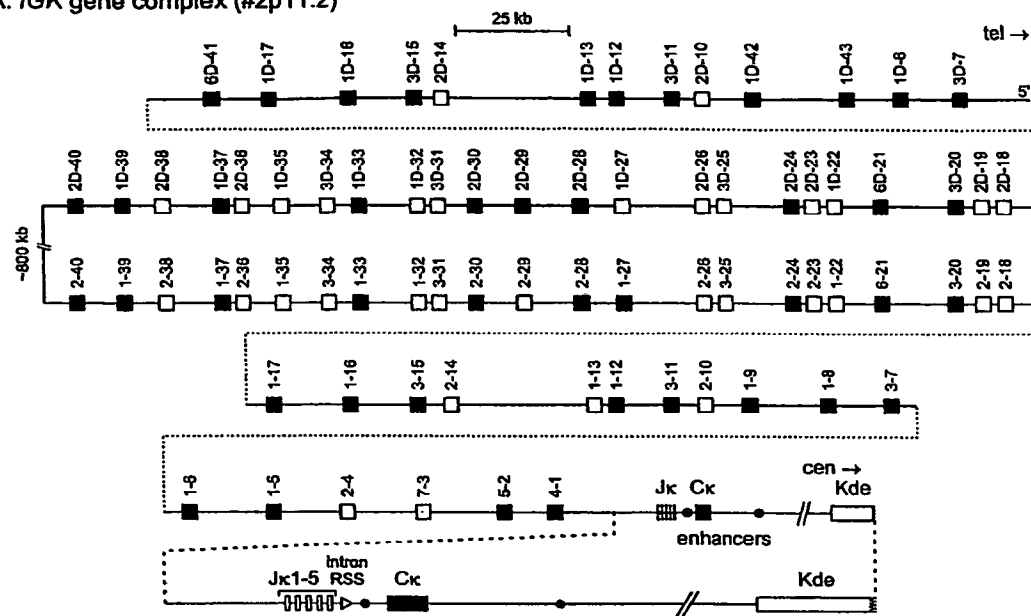


Figure 4 (A, B and C)

A. *IGK* gene complex (#2p11.2)

B

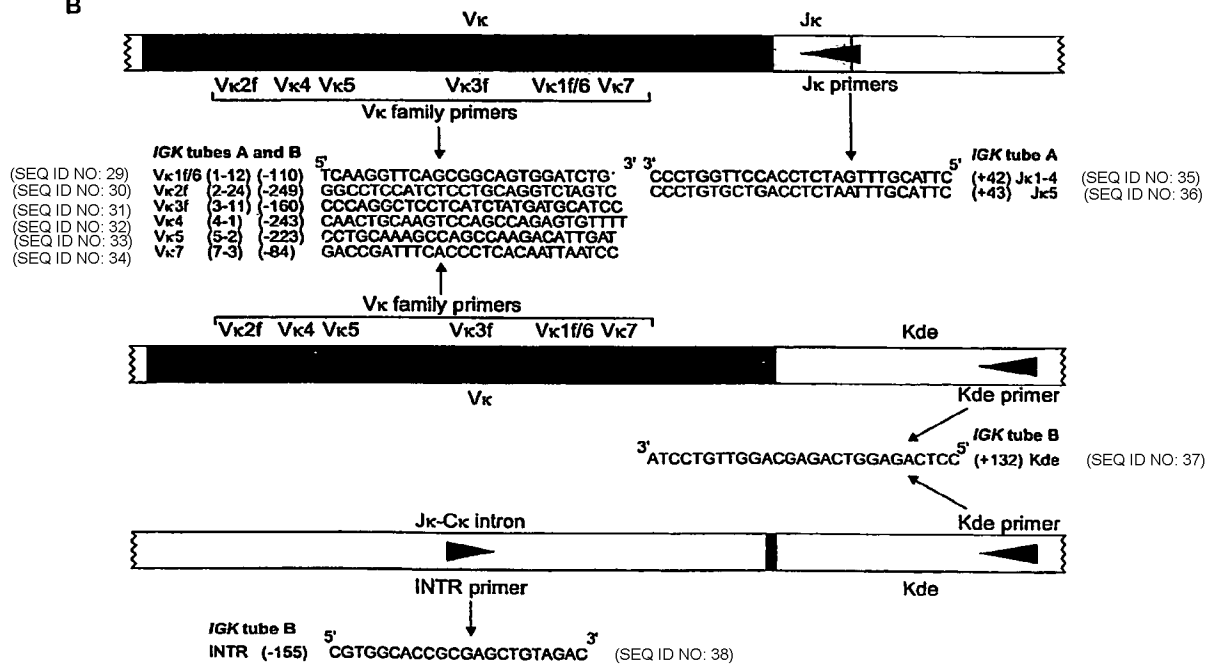
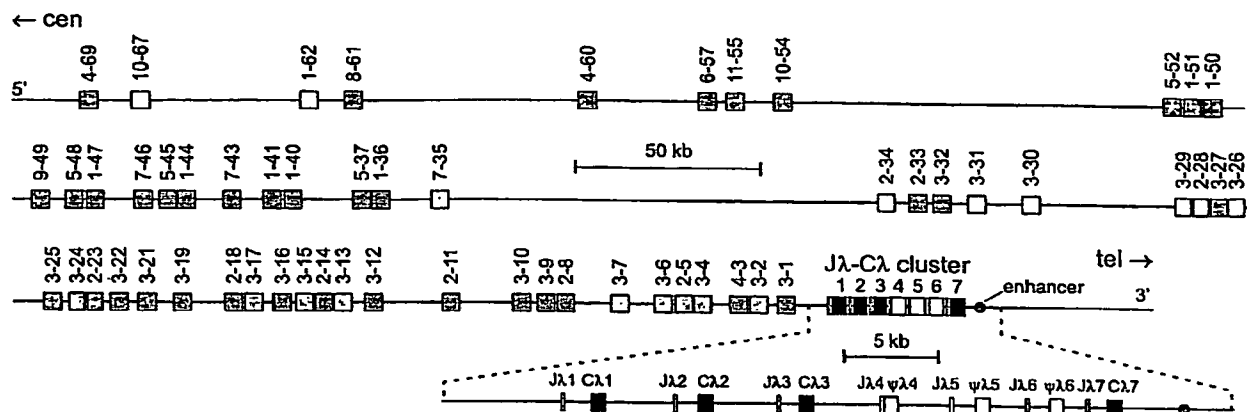


Figure 5 (A and B)

A. *IGL* gene complex (#22q11.2)

B

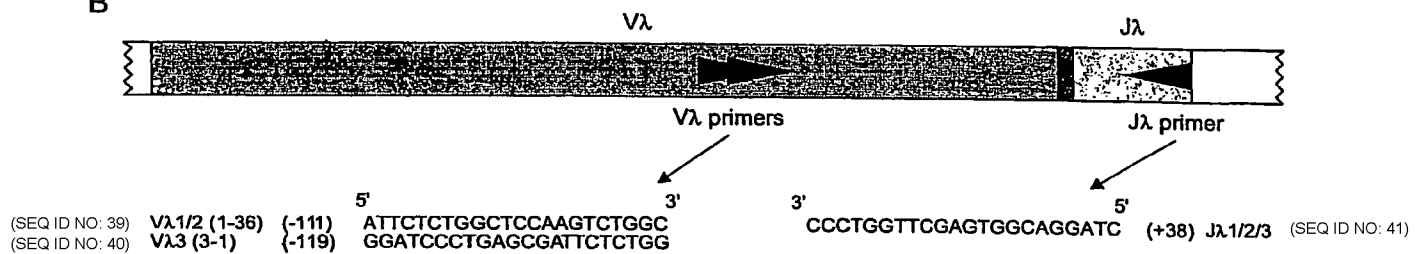
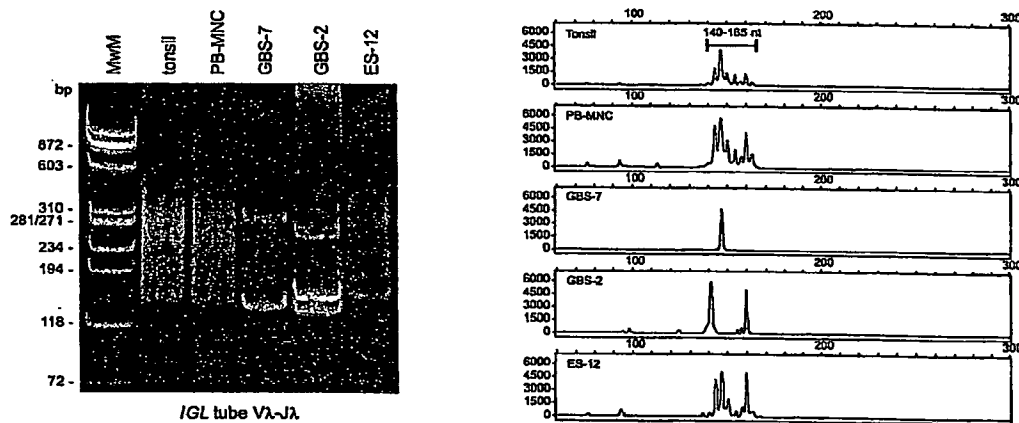
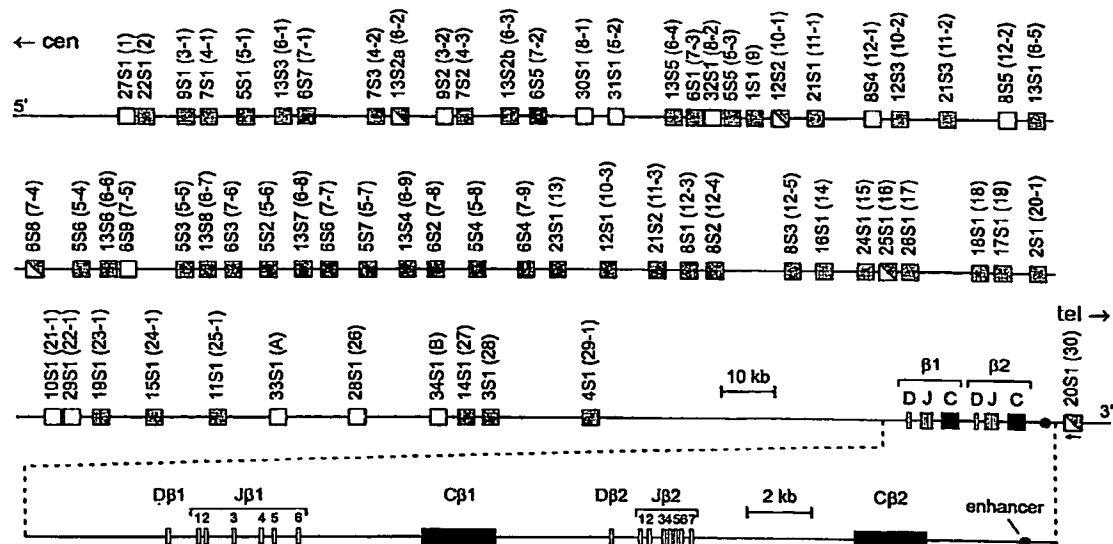
C. *IGL* tube Vλ-Jλ

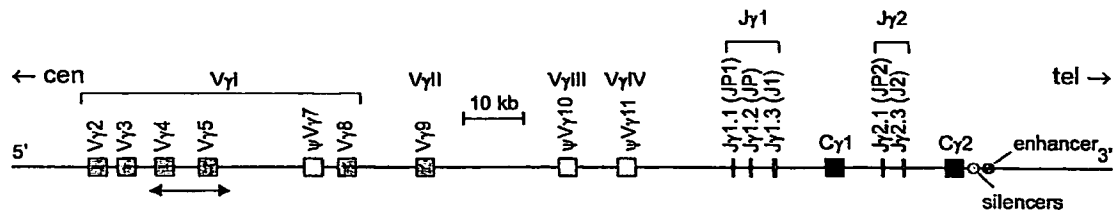
Figure 6 (A, B and C)

A. *TCRB* gene complex (#7q34)

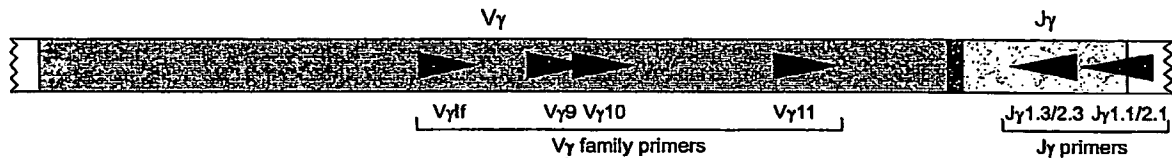
B



Figure 7 (A and B)

A. *TCRG* gene complex (#7p14)

B



TCRG tube A
 (SEQ ID NO: 80) Vγ1f (-178) 5' GGAAGGCCCCACAGCRTCCTT 3'
 (SEQ ID NO: 81) Vγ10 (-126) AGCATGGGTAAGACAAGCAA

TCRG tube B
 (SEQ ID NO: 82) Vγ9 (-141) CGGCACTGTCAGAAAGGAATC
 (SEQ ID NO: 83) Vγ11 (-58) CTCCACTTCCACTTTGAAA

TCRG tubes A and B
 (SEQ ID NO: 84) 3' CGAGTATCATTGAAGCGGACCATT 5' Jγ1.1/2.1 (JP1/2)
 (SEQ ID NO: 85) GAGAAACCGTCACCTTGTGTG (+38) Jγ1.3/2.3 (Jγ1/2)

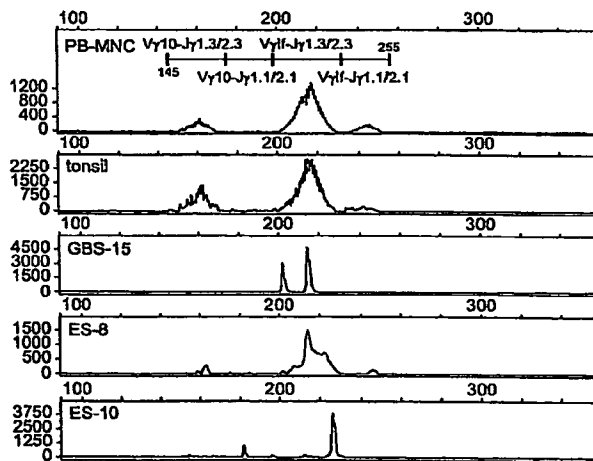
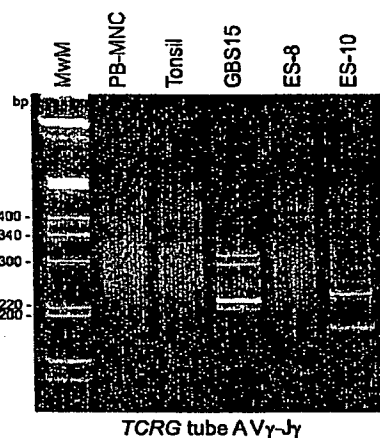
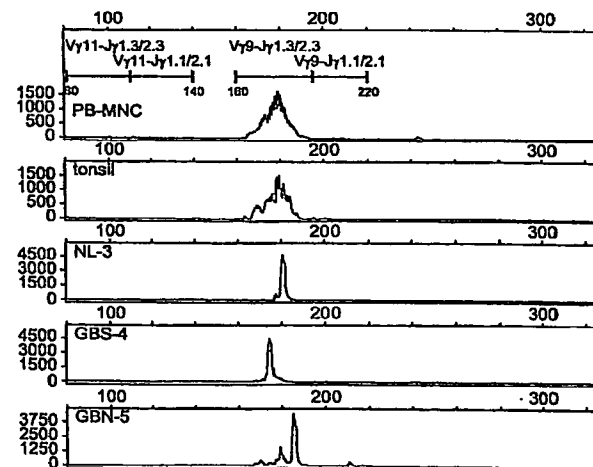
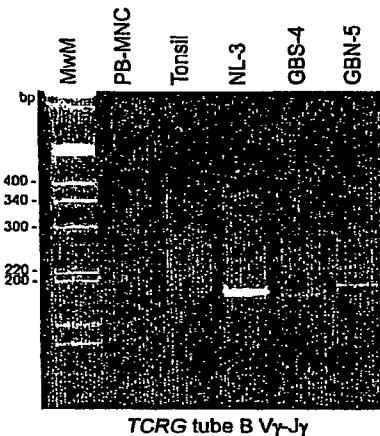
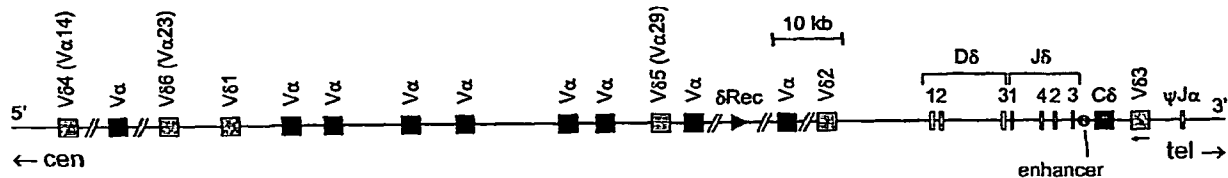
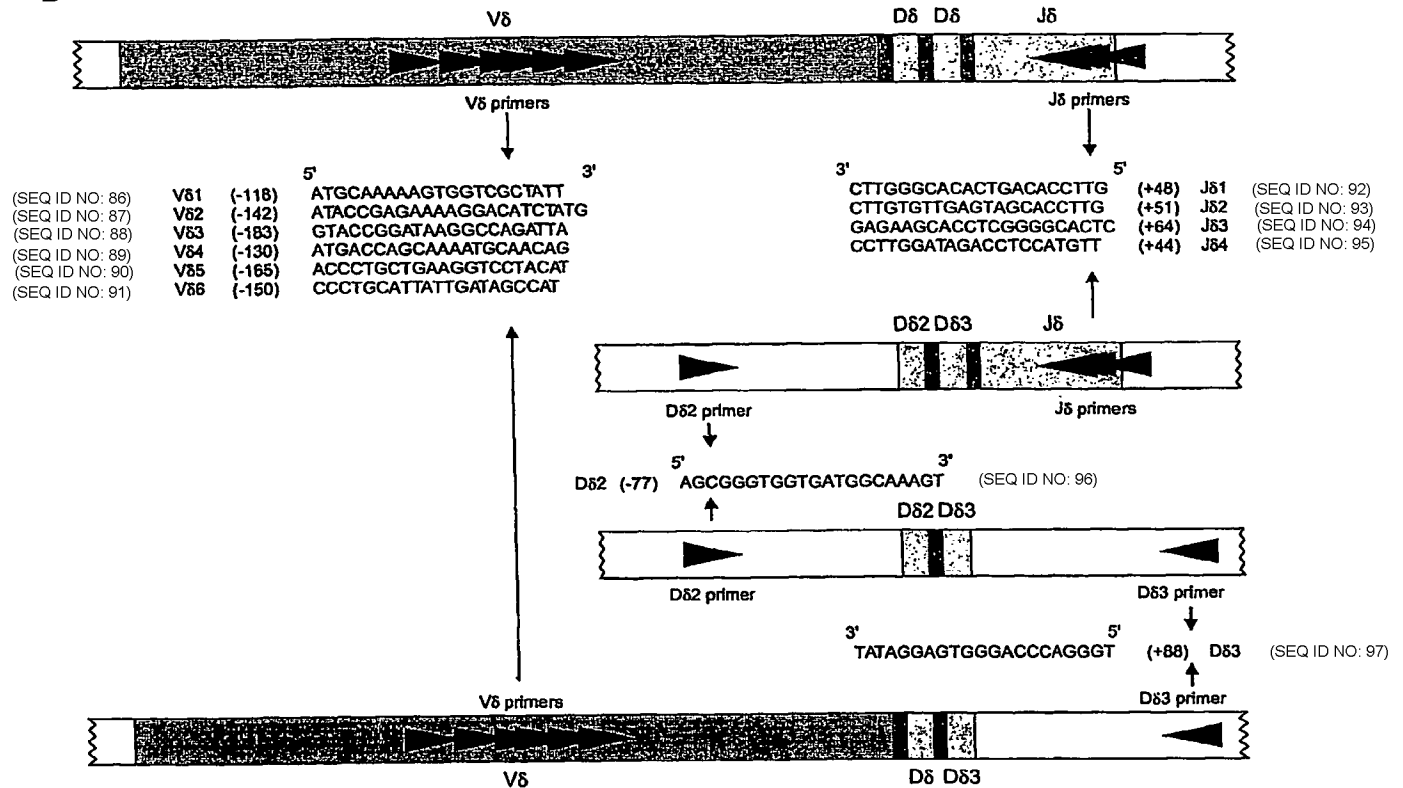
C. *TCRG* tube A Vγ-JγD. *TCRG* tube B Vγ-Jγ

Figure 8 (A, B, C, and D)

A. TCRD gene complex (#14q11.2)



B



C. TCRD tube Vδ-Jδ/Dδ-Dδ/Dδ-Jδ

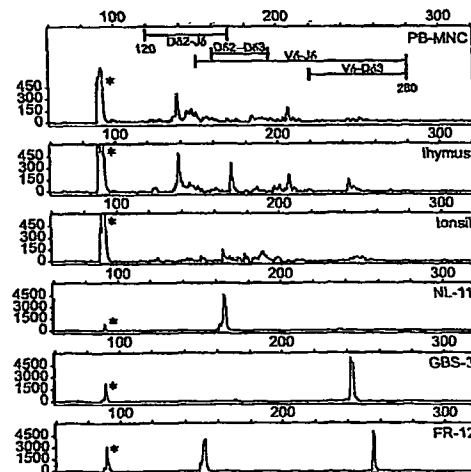
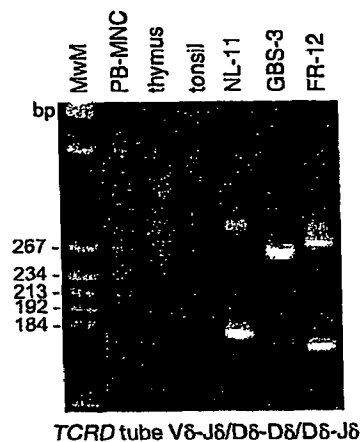


Figure 9 (A, B, and C)

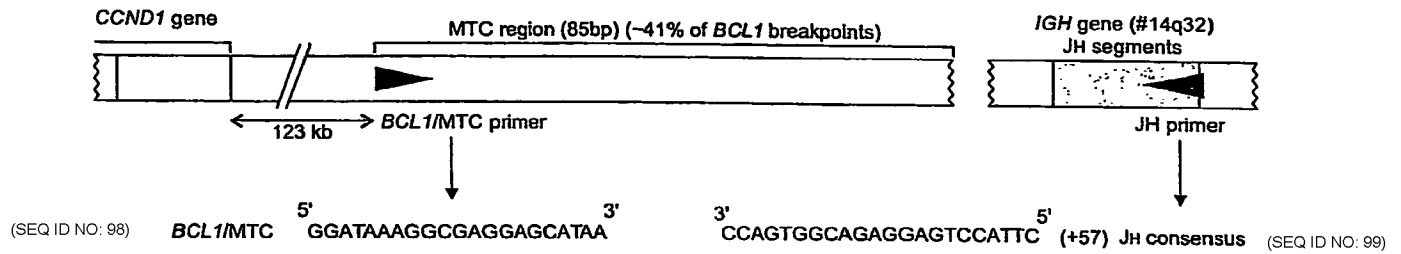
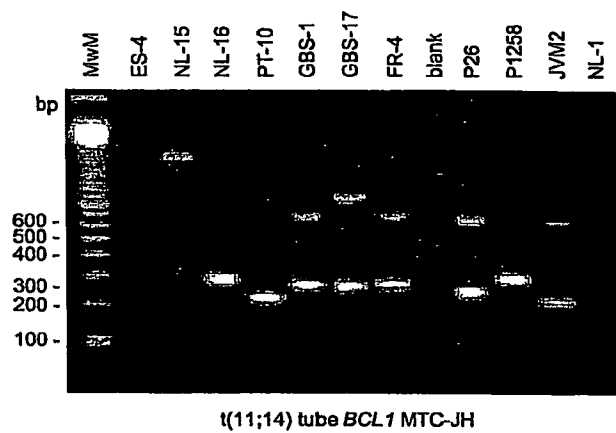
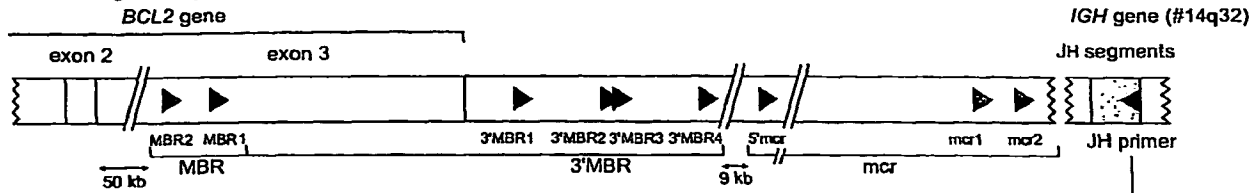
A. *BCL1* locus (#11q13)B. t(11;14) tube *BCL1* MTC-JH

Figure 10 (A and B)

A. *BCL-2* gene (#18q21)

(SEQ ID NO: 100)		t(14;18) tube A: MBR primers		5'		3'	3'		5'	t(14;18) tubes A, B, and C		(SEQ ID NO: 110)
(SEQ ID NO: 101)		MBR1	(3'end of exon 3) (-3072)	GACCAGCAGATTCAAATCTATGG						(+57)	JH consensus	
		MBR2	(3'end of exon 3) (-3575)	ACTCTGTGGCATTATGCATTATAT								
		t(14;18) tube B: 3'MBR primers										
(SEQ ID NO: 102)		3'MBR1	(3'end of exon 3) (+549)	GCACCTGCTGGATACAACACTG								
(SEQ ID NO: 103)		3'MBR2	(3'end of exon 3) (+1224)	AAACTAGCAGGGTGTGGTGGC (replaced by +1362; GGTGACAGAGCAAAACATGAACA)							(SEQ ID NO: 109)	
(SEQ ID NO: 104)		3'MBR3	(3'end of exon 3) (+1819)	GTAATGACTGGGGAGCAAATCTT								
(SEQ ID NO: 105)		3'MBR4	(3'end of exon 3) (+2550)	ACTGGTTGGCGTGGTTTAGAGA								
		t(14;18) tube C: mcr primers										
(SEQ ID NO: 106)		5'mcr	(3'end of exon 3) (+15681)	CCTTCTGAAAGAAACGAAAGCA								
(SEQ ID NO: 107)		mcr1	(file AF275873) (+1981)	TAGAGCAAGCGCCCAATAAATA								
(SEQ ID NO: 108)		mcr2	(file AF275873) (+2407)	TGAATGCCATCTCAAATCCAA								

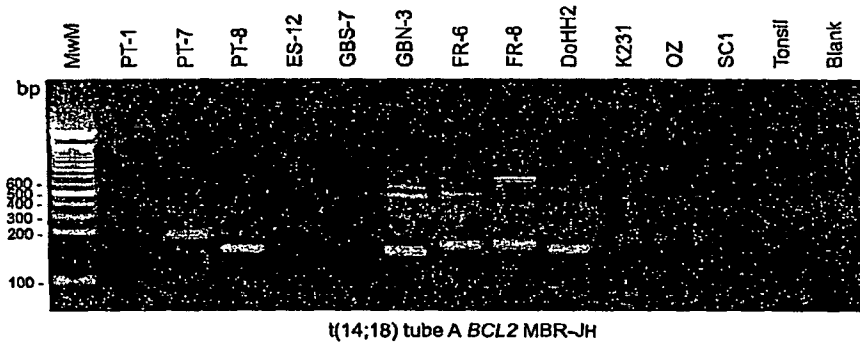
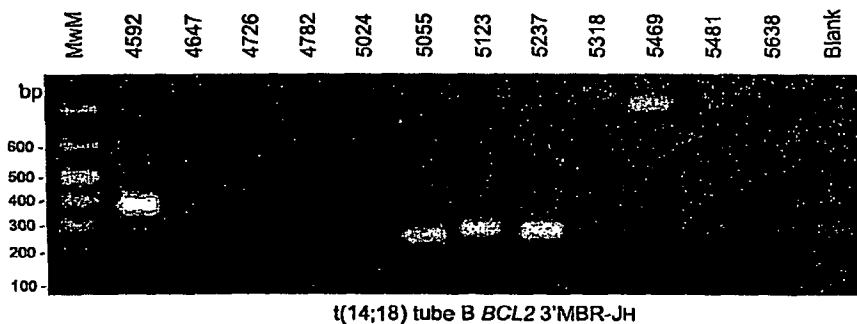
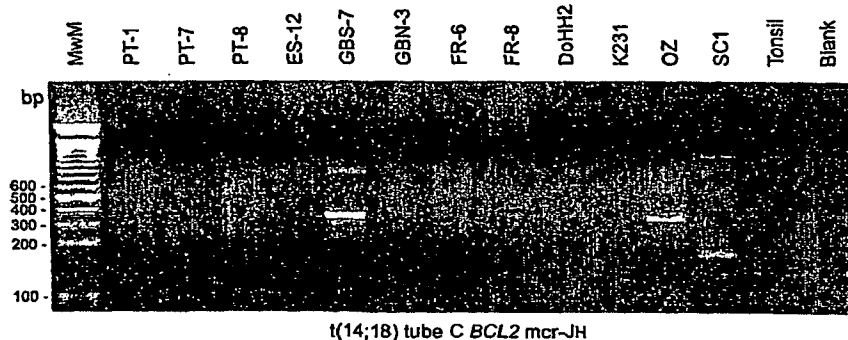
B. t(14;18) tube A *BCL2* MBR-JHC. t(14;18) tube B *BCL2* 3'MBR-JHD. t(14;18) tube C *BCL2* mcr-JH

Figure 11 (A, B, C, and D)

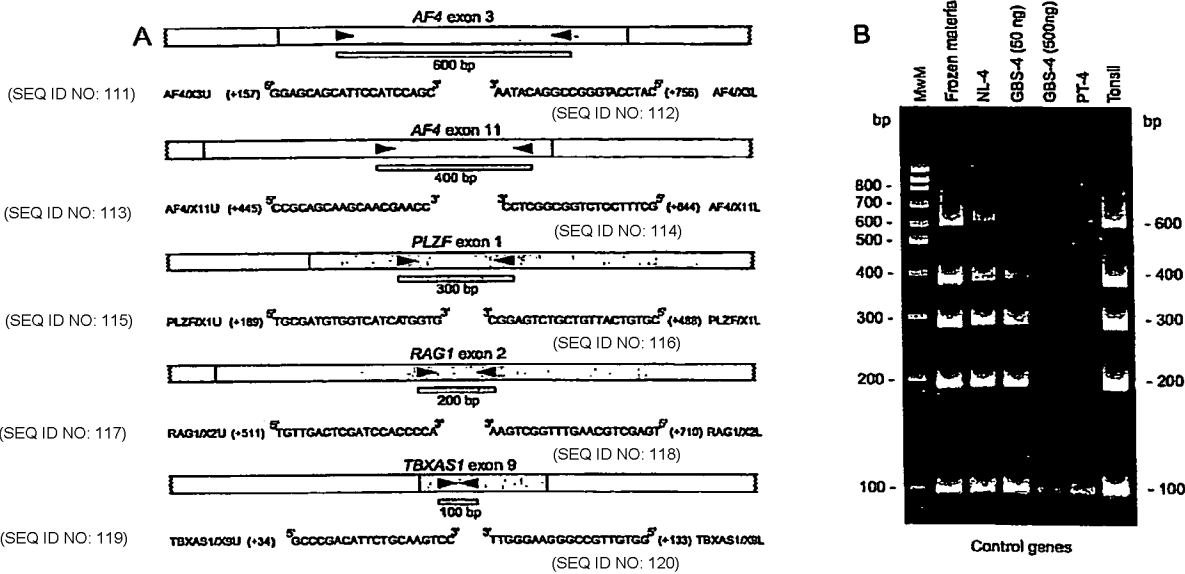


Figure 12 (A and B)